

SEQUENCE LISTING

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<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY4,
EXPRESSED HIGHLY IN PROSTATE, COLON, AND LUNG

<130> D0039NP/3053-4117US3

<140> TBA

<141> 2001-09-26

<150> 60/235,833

<151> 2000-09-27

<150> 60/261,776

<151> 2001-01-16

<150> 60/305,351

<151> 2001-07-13

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<151> 2001-08-17

<160> 60

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
20 25 30

Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
35 40 45

Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
50 55 60

Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
65 70 75 80

Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
85 90 95

Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
100 105 110

Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
115 120 125

Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
130 135 140

Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
145 150 155 160

Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
165 170 175

Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
180 185 190

Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
195 200 205

Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
210 215 220

Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
225 230 235 240

Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro
245 250 255

Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser
260 265 270

Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val
275 280 285

Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg
290 295 300

Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
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<212> DNA
<213> Homo sapiens

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cagaatataaa taaaatgaga taatcttagt taaaactata acttcctctt cagaactccc 420
aaccacattt gatctcagaa aaatactgtc ttcaaaatga cttctacaga gaagaaataa 480
ttttcccttggacacttagc acttaagggg aagattggaa gtaaagcctt gaaaagagta 540
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gcctagaaca taatagtgttatgcttatgcttgc accggttattt tttcatcaaa cctgattcc 1680
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gttacacaga gtaaatcacc agaaggctgg atttctgaaa aaactgtgca gagccaaacc 1920
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gtactattgt gtcaagtcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 2034

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
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tatggaagga atgtgtgacc 80

<210> 6
<211> 20
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic
oligos

<400> 6
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<210> 7
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<212> DNA
<213> Artificial Sequence

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oligos

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<211> 311
<212> PRT
<213> MOUSE

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Gly Leu Glu Met Ile His His Trp Ile Ser Ile Pro Phe Phe Val Ile
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Tyr Phe Ser Ile Ile Val Gly Asn Gly Thr Leu Leu Phe Ile Ile Trp
35 40 45
Ser Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Val Leu
50 55 60
Ala Ser Met Asp Leu Gly Met Thr Leu Thr Thr Met Pro Thr Val Leu
65 70 75 80
Gly Val Leu Val Leu Asn Gln Arg Glu Ile Val His Gly Ala Cys Phe
85 90 95
Ile Gln Ser Tyr Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Val
100 105 110
Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu
115 120 125
His Tyr Asn Ser Ile Leu Thr Asn Ser Arg Val Met Lys Met Ala Leu
130 135 140
Gly Ala Leu Leu Arg Gly Phe Val Ser Ile Val Pro Pro Ile Met Pro
145 150 155 160
Leu Phe Trp Phe Pro Tyr Cys His Ser His Val Leu Ser His Ala Phe
165 170 175
Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe
180 185 190
Asn Leu Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp
195 200 205
Ala Leu Ile Ile Ile Phe Ser Tyr Val Leu Ile Leu Lys Lys Val Met
210 215 220
Gly Ile Ala Ser Gly Glu Glu Arg Lys Lys Ser Leu Asn Thr Cys Val

225 230 235 240

Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu
245 250 255

Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile
260 265 270

Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile
275 280 285

Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Leu Arg Leu
290 295 300

Leu Ser Lys His Ser Arg Thr
305 310

<210> 9
<211> 307
<212> PRT
<213> MOUSE

<400> 9
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Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Ile
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Tyr Ile Ser Val Leu Leu Gly Asn Gly Thr Leu Leu Tyr Leu Ile Lys
35 40 45

Asp Asp His Asn Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
50 55 60

Ala Gly Thr Asp Leu Thr Val Thr Leu Thr Thr Met Pro Thr Val Met
65 70 75 80

Ala Val Leu Trp Val Asn His Arg Glu Ile Arg His Gly Ala Cys Phe
85 90 95

Leu Gln Ala Tyr Ile Ile His Ser Leu Ser Ile Val Glu Ser Gly Val
100 105 110

Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu
115 120 125

<210> 10
<211> 312
<212> PRT
<213> HUMAN

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1 5 10 15

Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Val
20 25 30

Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Leu Ile Lys
35 40 45

His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu
50 55 60

Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met
65 70 75 80

Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe
85 90 95

Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser
100 105 110

Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu
115 120 125

Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val
130 135 140

Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg
145 150 155 160

Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe
165 170 175

Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe
180 185 190

Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp
195 200 205

Ser Leu Ile Ile Leu Phe Ser Tyr Ile Leu Ile Leu Asn Thr Val Ile
210 215 220

Gly Ile Ala Ser Gly Glu Glu Gln Thr Lys Ala Leu Asn Thr Cys Val
225 230 235 240

Ser His Phe Cys Ala Val Leu Ile Phe Tyr Ile Pro Leu Ala Gly Leu
245 250 255

Ser Ile Ile His Arg Tyr Gly Arg Asn Ala Pro Pro Ile Ser His Ala
260 265 270

Val Met Ala Asn Val Tyr Leu Phe Val Pro Pro Ile Leu Asn Pro Val
275 280 285

Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr Gly Ile Ile Arg Leu
290 295 300

Leu Ser Lys His Arg Phe Ser Arg
305 310

<210> 11
<211> 319
<212> PRT
<213> CHICKEN

<400> 11
Met Tyr Pro Arg Asn Ser Ser Gln Ala Gln Pro Phe Leu Leu Ala Gly
1 5 10 15

Leu Pro Gly Met Ala Gln Phe His His Trp Val Phe Leu Pro Phe Gly
20 25 30

Leu Met Tyr Leu Val Ala Val Leu Gly Asn Gly Thr Ile Leu Leu Val
35 40 45

Val Arg Val His Arg Gln Leu His Gln Pro Met Tyr Tyr Phe Leu Leu
50 55 60

Met Leu Ala Thr Thr Asp Leu Gly Leu Thr Leu Ser Thr Leu Pro Thr
65 70 75 80

Val Leu Arg Val Phe Trp Leu Gly Ala Met Glu Ile Ser Phe Pro Ala
85 90 95

Cys Leu Ile Gln Met Phe Cys Ile His Val Phe Ser Phe Met Glu Ser
100 105 110

Ser Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Cys
115 120 125

Pro Leu Arg Tyr Ser Ser Ile Leu Thr Gly Ala Arg Val Ala Gln Ile
130 135 140

Gly Leu Gly Ile Ile Cys Arg Cys Thr Leu Ser Leu Leu Pro Leu Ile
145 150 155 160

Cys Leu Leu Thr Trp Leu Pro Phe Cys Arg Ser His Val Leu Ser His
165 170 175

Pro Tyr Cys Leu His Gln Asp Ile Ile Arg Leu Ala Cys Thr Asp Ala

180	185	190
Thr Leu Asn Ser Leu Tyr Gly Leu Ile Leu Val Leu Val Ala Ile Leu		
195	200	205
Asp Phe Val Leu Ile Ala Leu Ser Tyr Ile Met Ile Phe Arg Thr Val		
210	215	220
Leu Gly Ile Thr Ser Lys Glu Glu Gln Thr Lys Ala Leu Asn Thr Cys		
225	230	235
Val Ser His Phe Cys Ala Val Leu Ile Phe Tyr Ile Pro Leu Ala Gly		
245	250	255
Leu Ser Ile Ile His Arg Tyr Gly Arg Asn Ala Pro Pro Ile Ser His		
260	265	270
Ala Val Met Ala Asn Val Tyr Leu Phe Val Pro Pro Ile Leu Asn Pro		
275	280	285
Val Leu Tyr Ser Met Lys Ser Lys Ala Ile Cys Lys Gly Leu Leu Arg		
290	295	300
Leu Leu Cys Gln Arg Ala Ala Trp Pro Gly His Ala Gln Asn Cys		
305	310	315
<210> 12		
<211> 320		
<212> PRT		
<213> RAT		
<400> 12		
Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Met Leu Ile Gly Ile		
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Pro Gly Leu Glu Glu Ala His Phe Trp Phe Gly Phe Pro Leu Leu Ser		
20	25	30
Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val		
35	40	45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met		
50	55	60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile		
65	70	75
		80

Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys
85 90 95

Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
100 105 110

Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
115 120 125

Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly
130 135 140

Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Pro Leu Pro Leu
145 150 155 160

Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
165 170 175

Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu
180 185 190

Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
195 200 205

Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val
210 215 220

Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
225 230 235 240

Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
245 250 255

Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His
260 265 270

Val Leu Met Gly Asp Val Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
275 280 285

Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
290 295 300

Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr
305 310 315 320

<210> 13
<211> 321
<212> PRT
<213> MOUSE

<400> 13

Met	Asn	Ser	Lys	Ala	Ser	Met	Leu	Gly	Thr	Asn	Phe	Thr	Ile	Ile	His
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Pro Thr Val Phe Ile Leu Leu Gly Ile Pro Gly Leu Glu Gln Tyr His

20															30
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Thr Trp Leu Ser Ile Pro Phe Cys Leu Met Tyr Ile Ala Ala Val Leu

35															45
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Gly Asn Gly Ala Leu Ile Leu Val Val Leu Ser Glu Arg Thr Leu His

50															60
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Glu Pro Met Tyr Val Phe Leu Ser Met Leu Ala Gly Thr Asp Ile Leu

65															80
	70														

Leu Ser Thr Thr Val Pro Lys Thr Leu Ala Ile Phe Trp Phe His

85															95
		90													

Ala Gly Glu Ile Pro Phe Asp Ala Cys Ile Ala Gln Met Phe Phe Ile

100															110
		105													

His Val Ala Phe Val Ala Glu Ser Gly Ile Leu Leu Ala Met Ala Phe

115															125
		120													

Asp Arg Tyr Val Ala Ile Cys Thr Pro Leu Arg Tyr Ser Ala Val Leu

130															140
		135													

Thr Pro Met Ala Ile Gly Lys Met Thr Leu Ala Ile Trp Gly Arg Ser

145															160
		150													

Ile Gly Thr Ile Phe Pro Ile Ile Phe Leu Leu Lys Arg Leu Ser Tyr

165															175
			170												

Cys Arg Thr Asn Val Ile Pro His Ser Tyr Cys Glu His Ile Gly Val

180															190
				185											

Ala Arg Leu Ala Cys Ala Asp Ile Thr Val Asn Ile Trp Tyr Gly Phe

195															205
				200											

Ser Val Pro Met Ala Ser Val Leu Val Asp Val Ala Leu Ile Gly Ile

210															220
				215											

Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe Arg Leu Pro Ser Gln Asp
225 230 235 240

Ala Arg His Lys Ala Leu Asn Thr Cys Gly Ser His Ile Gly Val Ile
245 250 255

Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr Phe Leu Thr His Arg Phe
260 265 270

Gly Lys Asn Ile Pro His His Val His Ile Leu Leu Ala Asn Leu Tyr
275 280 285

Val Leu Val Pro Pro Met Leu Asn Pro Ile Ile Tyr Gly Ala Lys Thr
290 295 300

Lys Gln Ile Arg Asp Ser Met Thr Arg Met Leu Ser Val Val Trp Lys
305 310 315 320

Ser

<210> 14

<211> 326

<212> PRT

<213> MOUSE

<400> 14

Met Lys Val Ala Ser Ser Phe His Asn Asp Thr Asn Pro Gln Asp Val
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Trp Tyr Val Leu Ile Gly Ile Pro Gly Leu Glu Asp Leu His Ser Trp
20 25 30

Ile Ala Ile Pro Ile Cys Ser Met Tyr Ile Val Ala Val Ile Gly Asn
35 40 45

Val Leu Leu Ile Phe Leu Ile Val Thr Glu Arg Ser Leu His Glu Pro
50 55 60

Met Tyr Phe Phe Leu Ser Met Leu Ala Leu Ala Asp Leu Leu Leu Ser
65 70 75 80

Thr Ala Thr Ala Pro Lys Met Leu Ala Ile Phe Trp Phe His Ser Arg
85 90 95

Gly Ile Ser Phe Gly Ser Cys Val Ser Gln Met Phe Phe Ile His Phe

100 105 110
Ile Phe Val Ala Glu Ser Ala Ile Leu Leu Ala Met Ala Phe Asp Arg
115 120 125

Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Ser
130 135 140

Ser Val Ile Gly Lys Ile Gly Thr Ala Ala Val Val Arg Ser Phe Leu
145 150 155 160

Ile Cys Phe Pro Phe Ile Phe Leu Val Tyr Arg Leu Leu Tyr Cys Gly
165 170 175

Lys His Ile Ile Pro His Ser Tyr Cys Glu His Met Gly Ile Ala Arg
180 185 190

Leu Ala Cys Asp Asn Ile Thr Val Asn Ile Ile Tyr Gly Leu Thr Met
195 200 205

Ala Leu Leu Ser Thr Gly Leu Asp Ile Leu Leu Ile Ile Ser Tyr
210 215 220

Thr Met Ile Leu Arg Thr Val Phe Gln Ile Pro Ser Trp Ala Ala Arg
225 230 235 240

Tyr Lys Ala Leu Asn Thr Cys Gly Ser His Ile Cys Val Ile Leu Leu
245 250 255

Phe Tyr Thr Pro Ala Phe Phe Ser Phe Phe Ala His Arg Phe Gly Gly
260 265 270

Lys Thr Val Pro Arg His Ile His Ile Leu Val Ala Asn Leu Tyr Val
275 280 285

Val Val Pro Pro Met Leu Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys
290 295 300

Gln Ile Gln Asp Arg Val Val Phe Leu Phe Ser Ser Val Ser Thr Cys
305 310 315 320

Gln His Asp Ser Arg Cys
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<210> 15

<211> 318

<212> PRT

<213> MOUSE

<400> 15

Met Ser Pro Gly Asn Ser Ser Trp Ile His Pro Ser Ser Phe Leu Leu
1 5 10 15

Leu Gly Ile Pro Gly Leu Glu Leu Gln Phe Trp Leu Gly Leu Pro
20 25 30

Phe Gly Thr Val Tyr Leu Ile Ala Val Leu Gly Asn Val Ile Ile Leu
35 40 45

Phe Val Ile Tyr Leu Glu His Ser Leu His Gln Pro Met Phe Tyr Leu
50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Leu Gly Leu Ser Thr Ala Thr Val
65 70 75 80

Pro Arg Ala Leu Gly Ile Phe Trp Phe Gly Phe His Lys Ile Ala Phe
85 90 95

Arg Asp Cys Val Ala Gln Met Phe Phe Ile His Leu Phe Thr Gly Ile
100 105 110

Glu Thr Phe Met Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile
115 120 125

Cys Asn Pro Leu Arg Tyr Asn Thr Ile Leu Thr Asn Arg Thr Ile Cys
130 135 140

Ile Ile Val Gly Val Gly Leu Phe Lys Asn Phe Ile Leu Val Phe Pro
145 150 155 160

Leu Ile Phe Leu Ile Leu Arg Leu Ser Phe Cys Gly His Asn Ile Ile
165 170 175

Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Val
180 185 190

Ser Ile Lys Val Asn Val Leu Phe Gly Leu Ile Leu Ile Ser Met Ile
195 200 205

Leu Leu Asp Val Val Leu Ser Ala Leu Ser Tyr Ala Lys Ile Leu His
210 215 220

Ala Val Phe Lys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn
225 230 235 240

Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Phe Thr Pro Ala
245 250 255

Phe Phe Ser Phe Leu Thr His Arg Phe Gly His Asn Ile Pro Arg Tyr
260 265 270

Ile His Ile Leu Leu Ala Asn Leu Tyr Val Ile Ile Pro Xaa Ala Leu
275 280 285

Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Asp Arg Ala
290 295 300

Val Thr Ile Leu Cys Asn Glu Val Gly Gln Leu Ala Asp Asp
305 310 315

<210> 16

<211> 316

<212> PRT

<213> MOUSE

<400> 16

Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro Ser Val Leu Thr Leu
1 5 10 15

Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys Trp Ile Gly Ile Pro
20 25 30

Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly Asn Ser Leu Ile Leu
35 40 45

Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile Pro Met Tyr Ile Phe
50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu Ser Thr Cys Ile Leu
65 70 75 80

Pro Lys Met Leu Gly Ile Phe Trp Phe His Met Pro Gln Ile Ser Phe
85 90 95

Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His Ser Phe Gln Ala Thr
100 105 110

Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
115 120 125

Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser Pro Gln Leu Thr Thr
130 135 140

Cys Leu Gly Ala Gly Ala Leu Leu Arg Ser Leu Ile Thr Thr Phe Pro
145 150 155 160

Leu Ile Leu Leu Ile Lys Phe Cys Leu Lys Tyr Phe Arg Thr Thr Ile
165 170 175

Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala
180 185 190

Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu Leu Val Ala Phe Ala
195 200 205

Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe Ser Tyr Val Arg Ile
210 215 220

Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala
225 230 235 240

Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu
245 250 255

Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ala His Ile Pro
260 265 270

Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr Leu Leu Val Pro Pro
275 280 285

Phe Leu Asn Pro Ile Val Tyr Gly Ile Lys Thr Lys Gln Ile Arg Asp
290 295 300

Gln Val Leu Lys Met Phe Phe Ser Lys Lys Pro Leu
305 310 315

<210> 17
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 17
Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1 5 10 15

Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln

20

25

<210> 18

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 18

Arg Thr Glu His Ser Leu His Glu Pro Met Tyr

1

5

10

<210> 19

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 19

Asn Ser Thr Thr Ile Gln Phe Asp Ala Cys Leu Leu Gln Met

1

5

10

<210> 20

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 20

His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr Lys

1

5

10

15

<210> 21

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 21

Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu Ser His Ser Tyr Cys
1 5 10 15

Leu His Gln Asp Val Met Lys Leu Ala Cys Asp Asp Ile Arg

20 25 30

<210> 22

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 22

Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala
1 5 10

<210> 23

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 23

His Arg Phe Ser Lys Arg Arg Asp Ser Pro
1 5 10

<210> 24

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 24

Lys Thr Lys Glu Ile Arg Gln Arg Ile Leu Arg Leu Phe His Val Ala
1 5 10 15

Thr His Ala Ser Glu Pro
20

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Forward GPCR9
primer-

<400> 25

cctgtgctca acccaattgt ct

22

<210> 26

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reverse GPCR9
primer-

<400> 26

actgacacct agggctctga ag

22

<210> 27

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-F3
forward primer

<400> 27

agccgagcca catcgct

17

<210> 28
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GAPDH-R1
reverse primer

<400> 28
gtgaccaggc gcccaatac

19

<210> 29
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GAPDH-PVIC
Taqman(R) Probe

<400> 29
caaatatccgtt gactccgacc ttcacacctt

28

<210> 30
<211> 39
<212> DNA
<213> Artificial Sequence

<400> 30
cccaagcttg caccatgatg gtggatccca atggcattt

39

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HGPRBMY4 3'
primer

<400> 31

gaagatctct agggctctga agcgtgtgtg gcc

33

<210> 32
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HGPRBMY4 3'
primer- Flag tag

<400> 32
gaagatctct acttgcgtc gtcgtcattt tagtccatgg gctctgaagc gtgtgtggc 59

<210> 33
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 33
Met Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro Leu
1 5 10

<210> 34
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 34
Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe
1 5 10

<210> 35
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 35

Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr
1 5 10

<210> 36

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 36

Ala Ile His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu
1 5 10

<210> 37

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 37

His Arg Phe Ser Lys Arg Arg Asp Ser Pro Leu Pro Val Ile
1 5 10

<210> 38

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 38

Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1 5 10

<210> 39
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 39
Ile Ala Val Leu Gly Asn Leu Thr Ile Ile Tyr Ile Val Arg
1 5 10

<210> 40
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 40
Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe Asp Ala
1 5 10

<210> 41
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 41
Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile Leu
1 5 10 15

<210> 42
<211> 16

> <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 42

Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
1 5 10 15

<210> 43

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 43

Ile His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala
1 5 10 15

<210> 44

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 44

Gln Ala Lys Ala Phe Gly Thr Cys Val Ser His Val Cys Ala Val Phe
1 5 10 15

<210> 45

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 45
His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe
1 5 10 15

Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg
20 25

<210> 46
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo 1;
N=A+G+C+T; K=C+G+T

<400> 46
cgaagcgtaa gggcccgagcc ggccnnknnk nnknnknnkn nknnknnknn knnknnknnk 60
nnknnknnkn nknnknnknn knnkccgggt ccgggcggc 99

<210> 47
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo 2;
N+A+G+C+T; V=C+A+G

<400> 47
aaaaggaaaa aagcgccgc vnnvnnvnnv nnvnnvnnvn nvnnvnnvnn vnnvnnvnnv 60
nnvnnvnnvn nvnnvnnvnn gccgccccgga cccgg 95

<210> 48
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 48
Pro Gly Pro Gly Gly

<210> 49
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 5'
Primer

<400> 49
gcagcagcgg ccgccaggcc ttggatttggccct tcccaattt 38

<210> 50
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 3'
Primer

<400> 50
gcagcagtcg acgggctctg aagcgtgtgtt ggccac 36

<210> 51
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 5'
Primer

<400> 51
gcagcagcgg ccgcattatgtt gtggatccca atggcaatg 39

<210> 52
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 3'
Primer

<400> 52

gcagcagtcg accttcactc catagacaat tgggttg

37

<210> 53

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 53

Gly Asp Phe Trp Tyr Glu Ala Cys Glu Ser Ser Cys Ala Phe Trp
1 5 10 15

<210> 54

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 54

Cys Leu Arg Ser Gly Thr Gly Cys Ala Phe Gln Leu Tyr Arg Phe
1 5 10 15

<210> 55

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 55

Phe Ala Gly Gln Ile Ile Trp Tyr Asp Ala Leu Asp Thr Leu Met
1 5 10 15

56
15
PRT
Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

56
Leu Ile Phe Phe Asp Ala Arg Asp Cys Cys Phe Asn Glu Gln Leu
1 5 10 15

57
15
PRT
Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

57
Leu Glu Trp Gly Ser Asp Val Phe Tyr Asp Val Tyr Asp Cys Cys
1 5 10 15

58
15
PRT
Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

58
Arg Ile Val Pro Asn Gly Tyr Phe Asn Val His Gly Arg Ser Leu
1 5 10 15

59
15
PRT
Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 59

Trp Glu Arg Ser Ser Ala Gly Cys Ala Asp Gln Gln Tyr Arg Cys
1 5 10 15

<210> 60

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 60

Tyr Phe Ser Asp Gly Glu Ser Phe Phe Glu Pro Gly Asp Cys Cys
1 5 10 15